

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5

DB 48 EREKE 52

RESULT 2

Q4JUL4
ID Q4JUL4 PRELIMINARY: PRT: 61 AA.
AC Q4JUL4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DE 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein NMA1295.
GN NMA1295.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=69599;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 22491, / SEROGROUP A / SEROTYPE 14A.
RX MEDLINE=2024556; PubMed=10741979.
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.P., Morelli G., Busham D., Brown D., Chillingworth T., Davies R.M., Davis F., Devlin K., Feilwell T., Hamlin N., Harty A.S., Jorgensen K., Leather S., Moule S., Mungall K., Quail M.A., Rajadurai M.A., Rutherford K.M., Simmonds M., Skilton J., Whitehead S., Spratt B.G., Barrell H.G., "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
RI Nature 404:502-506(2000).
RL EMBL: A162755; CAH84547.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 61 AA: 7525 MW: A029B40BFA5EFA49 CRC64;

Query Match 100.0%; Score 25; DB 16; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5

DB 32 EREKE 36

RESULT 3

064627
ID 064627 PRELIMINARY: PRT: 62 AA.
AC 064627
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DE 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
DE At2g18970 protein.
GN At2g18970.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN CV, COLUMBIA;
RX MEDLINE=20084487; PubMed=10617197;
RA Liu X., Kaul S., Rounsley S.D., Shea P.P., Renito M., Li, Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Hartstead M.E., Feldblum T.V., Buell C.R., Ketchum K.A., Lee J.J., Rounsley C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Maynard D., Tallon L.J., Gill J.E., Adams M.D., Carrera A., Gray J., Gray T.H., Goodman H.M., Somerville C.P., Schaffner G.P., Preuss D., Nielsen W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C., "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
RI Nature 402:761-768(1999).

QY 1 EREKE 5
DB 53 EREKE 57

RESULT 4

049518
ID 049518 PRELIMINARY: PRT: 66 AA.
AC 049518
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DE 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Hypothetical 8.1 kDa protein.
GN F2432.160 OR A14618500.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A., Bancroft I., Moses H.W., Mayer K., Schueller C.;
RX Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A., Moses H.W., Lemcke K., Mayer K.P.X.;
RX Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC EU Arabidopsis sequencing project;
RX Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: A1021710; CAA16730.1; -;
DR EMBL: A1161548; CAH78852.1; -;
KW Hypothetical protein.
SQ SEQUENCE 66 AA: 8086 MW: F850CDB9E8E06224 CRC64;

Query Match 100.0%; Score 25; DB 10; Length 66;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5

DB 19 EREKE 23

RESULT 5

048967
ID 048967 PRELIMINARY: PRT: 80 AA.
AC 048967
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Similar to serine protease RE (Fragment).
GN Mycoplasma capricolum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Entomoplasmatales; Entomoplasmataceae.
OX NCBI_TaxID=2095;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 27343(K12);
 FX MEDLINE-96059641; PubMed 7476192;
 RA Bork P., Ouzounis S., Casari G., Schneider R., Sander C., Dolan M.,
 R1 Gilbert W., Gillevet P.M.;
 "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
 its physiology."
 RL Mol. Microbiol. 16:955-967(1995).
 DR EMBL: Z33027; CAA83706.1; -;
 KW Protease.
 FT NON_TER 1 1
 FT NON_TER 80 80
 SQ SEQUENCE 80 AA: 9695 MW, AELCH755A1355ERC CR064,

Query Match 100.0%; Score 25; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 46 EREKE 50
 |||||

RESULT 6

Q8X0A8 PRELIMINARY; PRT; 84 AA.

ID Q8X0A8 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 9.6 kDa protein
 GN B14D6.200
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariatales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schullie U., Aign V., Hehseisel J., Brandt P., Fartmann B., Holland P.,
 RA Nyakatura G., Mewes H.W., Mandhaupt G.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DP PML: AL356173; CAB91729.2;
 KW Hypothetical protein.
 SQ SEQUENCE 84 AA: 897; MW, HCSIRHBFCH20HL5D CR064,

Query Match 100.0%; Score 25; DB 3; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 39 EREKE 43
 |||||

RESULT 7

Q91631 PRELIMINARY; PRT; 85 AA.

ID Q91631 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE XE2.1 protein (fragment).
 GN XE2.1.
 OS Xenopus laevis (African clawed frog)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Neuman T., Zuber M.X.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U35055; AAA78933.1; -;
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00010; HLH_1;
 DR SMART: SM00353; HLH; 1;
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 85 85
 SQ SEQUENCE 85 AA: 10083 MW, 0439875b72b6f66p CR064;

Query Match 100.0%; Score 25; DB 13; Length 85;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 3 EREKE 7
 |||||

RESULT 8

Q8TUZ2 PRELIMINARY; PRT; 92 AA.

ID Q8TUZ2 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Chorismate mutase.
 GN PHEA OR M1609.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STEIN-AM19 / DSM 6324 / JCM 9639;
 EX MEDLINE-21927647; PubMed-11930014;
 RA Shesher A., Mecheraya K.V., Makarova K.S., Polushin N.M.,
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Naitale D.A., Begonin I.R., Tarasov P.I., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;
 RL "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 and morphology of archaeal methanogens";
 RL Naitale D.A., Begonin I.R., Tarasov P.I., Wolf Y.I., Stetter K.O.,
 DE EMBL: A010456; AAM92822.1; -;
 KW Complete proteome.
 SQ SEQUENCE 92 AA: 10623 MW, 090FCAC0F49HFFER CR064;

Query Match 100.0%; Score 25; DB 17; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 47 EREKE 51
 |||||

RESULT 9

Q9BGY7 PRELIMINARY; PRT; 94 AA.

ID Q9BGY7 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Hypothetical 10.7 kDa protein.
 GN Macaca fascicularis (Grab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL LOBE LEFT;

KA Osada N., Hida M., Kusuda J., Tanuma K., Iseki K., Hirai M., Ierao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.,
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 libraries."
 KL Submitted (FEB-2001) to the EMBL/GenBank/DBP databases
 DR EMBL: AB055270; HAH21894.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 94 AA; 10698 MW; 14771AAC3543EABD CRC64;

Query Match 100.0%; Score 25; DB 6; Length 94;
 Best local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 DB 52 EREKE 56
 |||||

RESULT 10

Q9LGR8 PRELIMINARY; PRT; 104 AA.
 AC Q9LGR8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE P0462H08.20 protein.
 GN P0462H08.20.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 CX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.,
 RT "Oryza sativa Nipponbare(CA) genomic DNA, chromosome 1, PAC
 clone: P0462H08."
 KL Submitted (JUN-2000) to the EMBL/GenBank/DBP databases.
 DR EMBL: AP002525; BAH07997.1; -
 SQ SEQUENCE 104 AA; 11434 MW; A3DE6295G4CE76D CRC64;

Query Match 100.0%; Score 25; DB 10; Length 104;
 Best local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 DB 99 EREKE 103
 |||||

RESULT 11

Q9K1T3 PRELIMINARY; PRT; 106 AA.
 AC Q9K1T3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE SpoIIIG (Fragment).
 OS Clostridium sporosches.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 CX NCBI_TaxID=1509;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:20340963; PubMed:10878124;
 RA Arcuri E.F., Wiedmann M., Boor K.J.;
 RT "Phylogeny and functional conservation of Sigma E in endospore-forming
 bacteria."
 KL Microbiology 146:1593-1604(2000).
 DR EMBL: AF225466; AAF35486.1; -
 DR InterPro: IPR000943; Sigma_70.
 DR Pfam: PF00140; sigma70; 1.

FI NON_TER 1 1
 FT NON_TER 106 106
 SQ SEQUENCE 106 AA; 12446 MW; F5144CE29A70C153C CRC64;
 Query Match 100.0%; Score 25; DB 2; Length 106;
 Best local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 DB 82 EREKE 86
 |||||

RESULT 12

Q9UTJ4 PRELIMINARY; PRT; 111 AA.
 AC Q9UTJ4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Hypothetical coiled-coil protein.
 GN SPAC1556.05C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 CX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Saunders D., Harris D., Mbougaill R.C., Rajandream M.A., Barrell B.G.;
 RT Submitted (NOV-1999) to the EMBL/GenBank/DBP databases.
 DR EMBL: AL132984; CAB61216.1; -
 SQ SEQUENCE 111 AA; 13513 MW; C9C87C83E241568D CRC64;

Query Match 100.0%; Score 25; DB 3; Length 111;
 Best local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 DB 50 EREKE 54
 |||||

RESULT 13

Q9HH91 PRELIMINARY; PRT; 117 AA.
 AC Q9HH91;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 14.3 kDa protein.
 OS Sulfolobus islandicus.
 OC Plasmid pHEN7.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 CX NCBI_TaxID=44080;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HEN7H2;
 RA MEDLINE:20510146; PubMed:11054382;
 RA Peng X., Holz L., Zillig W., Garrett K.A., She Q.;
 RT "Evolution of the family of pRN plasmids and their integrase-mediated
 insertion into the chromosome of the crenarchaeum Sulfolobus
 J. Mol. Biol. 303:449-454(2000).
 DR EMBL: AJ294536; CAC15842.1; -
 KL Hypothetical protein; Plasmid.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 117 AA; 14348 MW; D4CC45252C1F78A1 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 117;
 Best local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: January 16, 2003, 16:55:37
 Job Time : 20.2143 secs

QY 1 EREKE 5
 ||||
 DB 112 EREKE 116

RESULT 14

QRT4X8

ID Q814X8 PRELIMINARY: PRT: 117 AA.
 AC Q814X8;
 DT 01-JUN-2002 (TRENBLREL: 21, Created)
 DT 01-JUN-2002 (TRENBLREL: 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL: 21, Last annotation update)
 DE Erythrocyte membrane protein 1 (Fragment).
 GN VAR.
 GS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID:5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:PH4;
 RX MEDLINE:21839615; PubMed:11849711;
 RA Fowler E.V., Peters J.M., Gattton M.H., Chen N., Cheng Q.;
 RT "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
 ET genes among Asia-Pacific isolates."
 RL Mol Biochem Parasitol. 120:117-126(2002).
 DR EMBL: AF054934; AAL11298.1; -.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13871 MW; BC1E0F0548B7BE58 CRC64;

Query Match

100.0%; Score 25; DB 5; Length 117.

Best Local Similarity 100.0%; Prod. No. 3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 ||||
 DB 18 EREKE 22

RESULT 15

075408

ID 075408 PRELIMINARY: PRT: 120 AA.
 AC 075408;
 DT 01-NOV-1998 (TRENBLREL: 08, Created)
 DT 01-NOV-1998 (TRENBLREL: 08, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL: 08, Last annotation update)
 DE Huntingtin interacting protein HYPK (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA Faber P.W., Barnes G.T., Srinidhi J., Chen J., Gusella J.F.,
 RA MacDonald M.R.;
 RT "Huntingtin interacts with a family of WW domain proteins."
 RL Hum. Mol. Genet. 0:0-0(1998).
 DR EMBL: AF049613; AAC26849.1; -.
 FT NON_TER 1
 FT NON_TER 120
 SQ SEQUENCE 120 AA; 13520 MW; 0CF2C487B3FE23108 CRC64;

Query Match

100.0%; Score 25; DB 4; Length 120.

Best Local Similarity 100.0%; Prod. No. 3.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 ||||
 DB 71 EREKE 75

